



SEQUENCE LISTING

<110> KERE, Juha

<120> NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA

<130> 0933-0214P

<140> US 10/681,199

<141> 2003-10-09

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 1263

<212> DNA

<213> Homo sapiens

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<223> coding sequence for human DYXC1 (cDNA)

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<213> Homo sapiens

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<222> (369)..(1628)

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ctaccgga atg cct ctt cag gtt agc gat tac agc tgg cag cag acg aag 410
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Thr Ala Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp
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acg gac gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca 506
Thr Asp Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro
          35             40             45

ttt tta ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc 554
Phe Leu Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser
      50             55             60

aaa gca aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa 602
Lys Ala Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys
      65             70             75

gaa gcg gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag 650
Glu Ala Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu
      80             85             90

atg atg caa aga att aga gaa aaa tct att tta caa gca caa gag aga 698
Met Met Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg
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gca aaa gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa 746
Ala Lys Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln
          115            120            125

aaa tac gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa 794
Lys Tyr Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys
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aaa ata gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gca 842
Lys Ile Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Ala
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ttg gaa gcc tgg aaa gaa tat caa aga aaa gct gag gag gag caa aaa aaa 890
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Arg	Asn	Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu		
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Lys	Leu	Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile		
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Lys	Ile	Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser		
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Gln	Val	Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg		
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Arg	Ala	Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu		
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Thr	Glu	Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg		
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Lys	Ala	His	Val	Arg	Arg	Gly	Thr	Ala	Phe	Cys	Gln	Leu	Glu	Leu	Tyr		
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gta	gaa	ggc	cta	cag	gat	tat	gaa	gcg	gca	ctt	aag	att	gat	cca	tcc	1562	
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gga aca gaa cta aaa tct taatgactat tagaagtaac taagtattgt 1658
Gly Thr Glu Leu Lys Ser
415          420

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aaggtagaat tttaaaataa aagatttata aataa 1993

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<212> PRT
<213> Homo sapiens

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu
35          40          45
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala
50          55          60
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala
65          70          75          80
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met
85          90          95
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys
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Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr
115         120         125
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile

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Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn 195 200 205		
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Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile 225 230 235 240		
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Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys 275 280 285		
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Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala 355 360 365		
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370 375 380		
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys 385 390 395 400		
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agg aat tgg gaa aac ata ttt cct gag aag tta aag gaa gac aga gtc	728
Arg Asn Trp Glu Asn Ile Phe Pro Glu Lys Leu Lys Glu Asp Arg Val	
215 220 225	
cct gcg cct cgc tcc gct ggc agt att caa atc agc ttt acc cct cga	776
Pro Ala Pro Arg Ser Ala Gly Ser Ile Gln Ile Ser Phe Thr Pro Arg	
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Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val Ala Glu Glu Glu Glu	
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Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala Met Ser Thr Asp Leu	
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Pro Glu Phe Phe Asp Leu Lys Glu Glu Arg Asn Pro Asp Trp Leu	
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Val Asp Ala Tyr Asn Leu Ala Ile Arg Leu Asn Cys Lys Ile Pro Leu	
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325 330 335	
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Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu Leu Leu Thr Pro Pro	
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375 380 385	

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Val Phe Cys Gly Glu Ser Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu
      35          40          45
Phe Glu Leu Phe Leu Tyr Ala Pro Ile Asp Asp Gly Lys Ser Lys Ala
      50          55          60
Lys Ile Gly Asn Asp Thr Ile Leu Phe Thr Leu Tyr Lys Lys Glu Pro
      65          70          75          80
Val Leu Trp Asp Ser Leu Ser Val Pro Gly Val Asp Lys Glu Met Met
      85          90          95
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Lys Ala Lys
      100          105          110
Glu Ala Thr Glu Ala Lys Ala Val Ala Lys Arg Glu Asp Gln Arg Tyr
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 Arg Lys Glu Lys Pro Leu Glu Gly Lys Gln Ala Glu Glu Thr Lys Ala
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 Leu Lys Pro Arg Gly Leu Pro Arg Lys Ala Pro Pro Thr Arg Leu Pro
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 Thr Arg Gly Arg Asn Trp Glu Asn Ile Phe Pro Glu Lys Leu Lys Glu
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 Asp Arg Val Pro Ala Pro Arg Ser Ala Gly Ser Ile Gln Ile Ser Phe
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 Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val Ala Glu
 245 250 255
 Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala Met Ser
 260 265 270
 Thr Asp Leu Pro Glu Phe Phe Asp Leu Lys Glu Glu Glu Arg Asn Pro
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<210> 6
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<212> DNA
<213> Homo sapiens

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<223> human DYXC1 chromosomal gene region, nucleotides
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ggaagtggag gttgcaatga gctgagatca tgccattgca ctctagcctg ggcaacaaga 17340
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<400> 12

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25

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<212> DNA

<213> Pan troglodytes

<220>

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gtc	ttt	ctg	tct	ctg	ccc	ctc	aaa	ggc	gtg	tgc	gtc	aga	gac	acg	gac	96
Val	Phe	Leu	Ser	Leu	Pro	Leu	Lys	Gly	Val	Cys	Val	Arg	Asp	Thr	Asp	
			20					25					30			

gtg	ttc	tgc	atg	gaa	aac	tat	ctg	aag	gtc	aac	ttt	cct	cca	ttt	tta	144
Val	Phe	Cys	Met	Glu	Asn	Tyr	Leu	Lys	Val	Asn	Phe	Pro	Pro	Phe	Leu	
		35					40					45				

ttt	gag	gca	ttt	ctt	tat	gct	ccc	ata	gac	gat	gag	agc	agc	aaa	gca	192
Phe	Glu	Ala	Phe	Leu	Tyr	Ala	Pro	Ile	Asp	Asp	Glu	Ser	Ser	Lys	Ala	
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aag	att	ggg	aat	gac	acc	att	gtc	ttc	acc	ttg	tat	aaa	aaa	gaa	gcg	240
Lys	Ile	Gly	Asn	Asp	Thr	Ile	Val	Phe	Thr	Leu	Tyr	Lys	Lys	Glu	Ala	
	65				70				75					80		

gcc	atg	tgg	gag	acc	ctt	tct	gtg	acg	ggg	gtt	gac	aaa	gag	atg	atg	288
Ala	Met	Trp	Glu	Thr	Leu	Ser	Val	Thr	Gly	Val	Asp	Lys	Glu	Met	Met	
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caa	aga	att	aga	gaa	aaa	tct	att	tta	caa	gca	caa	gag	aga	gca	aaa	336
Gln	Arg	Ile	Arg	Glu	Lys	Ser	Ile	Leu	Gln	Ala	Gln	Glu	Arg	Ala	Lys	
				100				105					110			

gaa	gct	aca	gaa	gca	aaa	gct	gca	gca	aag	cgg	gaa	gat	caa	aaa	tat	384
Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr	
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gca	cta	agt	gtc	atg	atg	aag	att	gaa	gaa	gaa	gag	agg	aaa	aaa	ata	432
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile	
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gaa	gat	atg	aaa	gaa	aat	gaa	cgg	ata	aaa	gcc	act	aaa	gaa	ttg	gaa	480
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Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln	
165 170 175	
aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa gaa aga	576
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	
180 185 190	
aaa aaa ata aaa tat aag agt ctt act aga aat ttg gca tct aga aat	624
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	
195 200 205	
ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta	672
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	
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aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc	720
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile	
225 230 235 240	
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta	768
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	
245 250 255	
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca	816
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	
260 265 270	
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Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	
275 280 285	
aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa	912
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	
290 295 300	
aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat	960
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn	
305 310 315 320	
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Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys	
325 330 335	
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Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu	
340 345 350	
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Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
355 360 365	
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His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	

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 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys
 385 390 395 400

att gta caa att gat gct gag aag att cgg aat gta att caa gga aca 1248
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gaa cta aaa tct taa 1263
 Glu Leu Lys Ser
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 <212> PRT
 <213> Pan troglodytes

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 35 40 45
 Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala
 50 55 60
 Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala
 65 70 75 80
 Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met
 85 90 95
 Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys
 100 105 110
 Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr
 115 120 125
 Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile
 130 135 140
 Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu
 145 150 155 160
 Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln
 165 170 175
 Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg
 180 185 190
 Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn
 195 200 205

Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu
 210 215 220
 Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile
 225 230 235 240
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 245 250 255
 Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala
 260 265 270
 Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys
 275 280 285
 Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu
 290 295 300
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn
 305 310 315 320
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys
 325 330 335
 Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu
 340 345 350
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala
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 370 375 380
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys
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 Glu Leu Lys Ser
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 <213> Gorilla gorilla

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu				
35 40 45				
ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca	192			
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala				
50 55 60				
aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg	240			
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala				
65 70 75 80				
gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg	288			
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met				
85 90 95				
caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa	336			
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys				
100 105 110				
gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat	384			
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr				
115 120 125				
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Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile				
130 135 140				
gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa	480			
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu				
145 150 155 160				
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Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Glu Ile Gln				
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aga gaa gag aag tta tgt caa aaa gaa aag caa att aaa gaa gaa aga	576			
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg				
180 185 190				
aaa aaa tta aaa tat aag agt ctt act aga aat ttg gca tct aga aat	624			
Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn				
195 200 205				
ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta	672			
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu				
210 215 220				
aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc	720			
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile				
225 230 235 240				

aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta	768
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	
245 250 255	
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca	816
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	
260 265 270	
atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa gaa aag	864
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	
275 280 285	
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Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	
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305 310 315 320	
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Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys	
325 330 335	
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa	1056
Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu	
340 345 350	
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca	1104
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
355 360 365	
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa	1152
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	
ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa	1200
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys	
385 390 395 400	
att gta caa att gat gct gag aag att cgg aat gta att caa gga aca	1248
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Glu Leu Lys Ser	
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<211> 420

<212> PRT

<213> Gorilla gorilla

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Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	50	55	60
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	65	70	75
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met	85	90	95
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	100	105	110
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr	115	120	125
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile	130	135	140
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu	145	150	155
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Glu Ile Gln	165	170	175
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	180	185	190
Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	195	200	205
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	210	215	220
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile	225	230	235
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	245	250	255
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	260	265	270
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	275	280	285
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	290	295	300
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn			

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Asn Lys Met Pro	Leu Leu Tyr Leu	Asn Arg Ala Ala Cys His	Leu Lys			
	325	330	335			
Leu Lys Asn Leu	His Lys Ala Ile	Glu Asp Ser Ser	Lys Ala Leu Glu			
	340	345	350			
Leu Leu Met Pro	Pro Val Thr Asp	Asn Ala Asn Ala Arg	Met Lys Ala			
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His Val Arg Arg	Gly Thr Ala Phe	Cys Gln Leu Glu	Leu Tyr Val Glu			
	370	375	380			
Gly Leu Gln Asp Tyr	Glu Ala Ala Leu	Lys Ile Asp Pro Ser	Asn Lys			
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 <222> (1)..(1260)

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Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp	
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gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta	144
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu	
35 40 45	
ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca	192
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	
50 55 60	
aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg	240
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	
65 70 75 80	
gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag acg atg	288
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met	

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caa	aga	att	aga	gaa	aaa	tct	att	tta	caa	gca	caa	gag	aga	gca	aaa	336				
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gaa	gct	aca	gaa	gca	aaa	gct	gca	gca	aag	cgg	gaa	gat	caa	aaa	tat	384				
Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr					
			115				120						125							
gca	cta	agt	gtc	atg	atg	aag	att	gaa	gaa	gaa	gag	agg	aaa	aaa	ata	432				
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile					
			130				135						140							
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			145				150						155							
gcc	tg	g	aaa	gaa	tat	caa	aga	aaa	gct	gag	gag	cac	aaa	aaa	att	528				
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Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg					
			180							185			190							
aaa	aaa	tta	aaa	tac	aag	agt	ctt	act	aga	aat	tcg	gca	tct	aga	aac	624				
Lys	Lys	Leu	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Ser	Ala	Ser	Arg	Asn					
			195				200						205							
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Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu					
			210				215						220							
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			225				230						235							
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Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val					
			245							250			255							
gca	gaa	gag	gag	gag	tg	cta	cac	aaa	caa	gct	gag	gca	cga	aga	gca	816				
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atg	aat	act	gac	ata	gct	gaa	ctt	tgc	gat	tta	aaa	gaa	gaa	gaa	aag	864				
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys					
			275				280						285							
aac	cca	gaa	tg	ttg	aag	gat	aaa	gga	aac	aaa	ttg	ttt	gca	aca	gaa	912				
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu					
			290				295						300							
aac	tat	ttg	gca	gct	atc	aat	gca	tat	aat	tta	gcc	ata	aga	cta	aat	960				
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn					
			305				310						315							

aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa	1008
Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys	
325 330 335	
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa	1056
Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu	
340 345 350	
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca	1104
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
355 360 365	
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa	1152
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	
ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa	1200
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys	
385 390 395 400	
att gta caa att gat gct gag aag att cgg aat gta att caa gga aca	1248
Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr	
405 410 415	
gaa cta aaa tct taa	1263
Glu Leu Lys Ser	
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 <212> PRT
 <213> Pongo pygmaeus

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu	
35 40 45	
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	
50 55 60	
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	
65 70 75 80	
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met	
85 90 95	
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	
100 105 110	

Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr	115	120	125	
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile	130	135	140	
Glu	Asp	Met	Lys	Glu	Asn	Glu	Arg	Ile	Lys	Ala	Thr	Lys	Glu	Leu	Glu	145	150	155	160
Ala	Trp	Lys	Glu	Tyr	Gln	Arg	Lys	Ala	Glu	Glu	His	Lys	Lys	Ile	Gln	165	170	175	
Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg	180	185	190	
Lys	Lys	Leu	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Ser	Ala	Ser	Arg	Asn	195	200	205	
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu	210	215	220	
Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile	225	230	235	240
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val	245	250	255	
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala	260	265	270	
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys	275	280	285	
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu	290	295	300	
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn	305	310	315	320
Asn	Lys	Met	Pro	Leu	Leu	Tyr	Leu	Asn	Arg	Ala	Ala	Cys	His	Leu	Lys	325	330	335	
Leu	Lys	Asn	Leu	His	Lys	Ala	Ile	Glu	Asp	Ser	Ser	Lys	Ala	Leu	Glu	340	345	350	
Leu	Leu	Met	Pro	Pro	Val	Thr	Asp	Asn	Ala	Asn	Ala	Arg	Met	Lys	Ala	355	360	365	
His	Val	Arg	Arg	Gly	Thr	Ala	Phe	Cys	Gln	Leu	Glu	Leu	Tyr	Val	Glu	370	375	380	
Gly	Leu	Gln	Asp	Tyr	Glu	Ala	Ala	Leu	Lys	Ile	Asp	Pro	Ser	Asn	Lys	385	390	395	400
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Glu Leu Lys Ser
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<213> Pan paniscus

<220>
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gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac acg gac 96
Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp
20 25 30

gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta 144
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu
35 40 45

ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca 192
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala
50 55 60

aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg 240
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala
65 70 75 80

gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg 288
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met
85 90 95

caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa 336
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys
100 105 110

gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat 384
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr
115 120 125

gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa aaa ata 432
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile
130 135 140

gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa 480
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu
145 150 155 160

gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa aaa att cag 528
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln

165								170					175					
aga	gaa	gag	aaa	tta	tgt	caa	aaa	gaa	aag	caa	att	aaa	gaa	gaa	aga	576		
Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg			
			180				185						190					
aaa	aaa	ata	aaa	tat	aag	agt	ctt	act	aga	aat	ttg	gca	tct	aga	aat	624		
Lys	Lys	Ile	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Leu	Ala	Ser	Arg	Asn			
			195				200						205					
ctt	gct	cca	aaa	ggg	aga	aat	tca	gaa	aat	ata	ttt	act	gag	aag	tta	672		
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu			
			210				215						220					
aag	gaa	gac	agt	att	cct	gct	cct	cgc	tct	gtt	ggc	agt	att	aaa	atc	720		
Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile			
			225				230						235					
aac	ttt	acc	cct	cga	gta	ttc	cca	aca	gct	ctt	cgt	gaa	tca	caa	gta	768		
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val			
			245				250						255					
gca	gaa	gag	gag	gag	tgg	ctg	cac	aaa	caa	gct	gag	gca	cga	aga	gca	816		
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala			
			260				265						270					
atg	aat	act	gac	ata	gct	gaa	ctt	tgc	gat	tta	aaa	gaa	gaa	gaa	aag	864		
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys			
			275				280						285					
aac	cca	gaa	tgg	ttg	aag	gat	aaa	gga	aac	aaa	ttg	ttt	gca	aca	gaa	912		
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu			
			290				295						300					
aac	tat	ttg	gca	gct	atc	aat	gca	tat	aat	tta	gcc	ata	aga	cta	aat	960		
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn			
			305				310						315					
aat	aag	atg	cca	cta	ttg	tat	ttg	aac	cgg	gct	gct	tgc	cac	cta	aaa	1008		
Asn	Lys	Met	Pro	Leu	Leu	Tyr	Leu	Asn	Arg	Ala	Ala	Cys	His	Leu	Lys			
			325				330						335					
cta	aaa	aac	tta	cac	aag	gct	att	gaa	gat	tct	tct	aag	gca	ctg	gaa	1056		
Leu	Lys	Asn	Leu	His	Lys	Ala	Ile	Glu	Asp	Ser	Ser	Lys	Ala	Leu	Glu			
			340				345						350					
tta	ttg	atg	cca	cct	gtt	aca	gac	aat	gct	aat	gca	aga	atg	aag	gca	1104		
Leu	Leu	Met	Pro	Pro	Val	Thr	Asp	Asn	Ala	Asn	Ala	Arg	Met	Lys	Ala			
			355				360						365					
cat	gta	cga	cgt	gga	aca	gca	ttc	tgt	caa	cta	gaa	ttg	tat	gta	gaa	1152		
His	Val	Arg	Arg	Gly	Thr	Ala	Phe	Cys	Gln	Leu	Glu	Leu	Tyr	Val	Glu			
			370				375						380					
ggc	cta	cag	gat	tat	gaa	gcg	gca	ctt	aag	att	gat	cca	tcc	aac	aaa	1200		
Gly	Leu	Gln	Asp	Tyr	Glu	Ala	Ala	Leu	Lys	Ile	Asp	Pro	Ser	Asn	Lys			
			385				390						395					

att gta caa att gat gct gag aag att cgg aat gta att caa gga aca	1248
Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr	
405 410 415	

gaa cta aaa tct taa	1263
Glu Leu Lys Ser	
420	

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu	
35 40 45	
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	
50 55 60	
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	
65 70 75 80	
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met	
85 90 95	
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	
100 105 110	
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr	
115 120 125	
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile	
130 135 140	
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu	
145 150 155 160	
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln	
165 170 175	
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	
180 185 190	
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	
195 200 205	
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	
210 215 220	

Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile
 225 230 235 240
 Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val
 245 250 255
 Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala
 260 265 270
 Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys
 275 280 285
 Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu
 290 295 300
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn
 305 310 315 320
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys
 325 330 335
 Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu
 340 345 350
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala
 355 360 365
 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu
 370 375 380
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys
 385 390 395 400
 Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr
 405 410 415
 Glu Leu Lys Ser
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 cacaccaaag tttgagaacc act 23

 <210> 24
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 <400> 24
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 <210> 25
 <211> 22
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<400> 34
ggaaattcta aaacatattc atgacg 26

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<210> 42

<211> 27

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<223> PCR Primer 126403-F

<400> 42

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27